

**AMENDMENT AFTER FINAL**  
**U.S. Appln. No. 09/915,543**

**REMARKS**

Claim 71 has been amended to correct an inadvertent and obvious typographical error.

In paragraph 2, on page 2 of the Office Action, the Examiner rejects Claims 71, 73, 75 and 77 and new Claims 79-82 under 35 U.S.C. 112, first paragraph as lacking written description.

The Examiner notes Applicants' request that the rejection be withdrawn on the grounds that the claims have been amended such that the claimed polypeptides do not contain both the HD1 and HD2 domains at the same time, and further that new Claims 79-82 require that the polypeptides bind to Doll or  $\beta$ -cat. However, the Examiner contends that contrary to Applicants' assertions, the scope of the Claims 71, 73, 75 and 77 includes polypeptides containing both the HD1 and HD2 domains in view of the expression "or" after sections (i) and (ii) of Claim 71.

In view of the amendment to Claim 71 to correct the obvious typographical error, i.e., the "or" should have been deleted, it is clear that the polypeptides of amended Claims 71, 73, 75 and 77 do not contain both the HD1 and HD2 domains at the same time. (It should be noted that Claims 79-82 do not contain the objected to "or".)

The Examiner further contends that the claims should be limited to polypeptides "consisting of" the recited residues, as these residues are not representative of the claimed genus of polypeptides "comprising" the claimed sequence because the genus is highly variable and the specification does not provide a description of which polypeptides within the genus have the function claimed, and also because there is no correlation

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between the structure provided and the claimed function (inhibition of the tcf-driven luciferase activity).

Applicants respectfully submit that the Examiner's rejection is improper, since it is not the function of the claims to exclude inoperative embodiments, but rather the function of claims is to recite the invention. The invention is the recited domains and polypeptides containing the same, but not polypeptides containing both domains, and which inhibits tcf-driving luciferase activity.

For example, as recited in Claims 73, 75, 80 and 81, additional polypeptides can be fused to the claimed polypeptides to form chimeric polypeptides. These additional polypeptides include reporter or targeting or tag polypeptides, e.g., an antigenic epitope, glutathione-S-transferase, thioredoxin, and antibody. These additional polypeptides are typical of those well-known in the art, and would not effect the basic activity of the claimed polypeptides. The present specification clearly provides a written description for such chimeric polypeptides (see, e.g., original Claims 20-21; page 6, lines 13-20; and page 28, lines 9-14 of the present specification). Figure 15B demonstrates that such fusion polypeptides, i.e., GFP-HD2, is effective at inhibiting tcf-driven luciferase activity.

Furthermore, it is not required that either the specification or the claims recite what additional amino acids can be added and still give rise to functional polypeptides, since such can be determined by routine experimentation. What is critical to the invention is the specific domains which give rise to the functional properties of the claimed polypeptide. The claims must merely recite the critical elements of the invention, and as the additional sequences which may or may not

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be present are not critical to the invention (as long as both the domains are not present at the same time), Applicants respectfully submit that it is improper for the Examiner to require Applicants to further limit the claims.

Moreover, contrary to the Examiner's contention there is a disclosed structural/functional relationship between the claimed residues and tcf-driven luciferase activity, as demonstrated in the Examples of the present specification. That is, e.g., Claim 79 states that peptide (i) binds to Doll; peptide (ii) binds to CAT and that polypeptides containing either, but not both peptides, inhibits tcf-driven luciferase activity. Further, Claim 79 recites that the peptides have at least 90% identity with the recited sequences. Support for such identity can be found, *inter alia*, at page 5, lines 13-14, of the present specification where 90% identity is in the evolutionary conserved domains shown in Figure 7, e.g., HD1 and HD2; page 7, lines 14-20, where it states that the invention relates to peptides comprising a homology domain described in Figure 7 useful to block Lgs function in cancer cells; and page 6, lines 3-7, where it is taught that the invention concerns an isolated Lgs polypeptide or a fragment thereof comprising at least 90% sequence identity with a sequence in the full length sequence. As the recited sequences contain no more than 34 amino acids, this means that at most there are only 3 amino acid substitutions within the peptides covered by the claims. Appropriate substitutions can be routinely determined using the assays described in the specification for binding Doll or CAT, and for inhibiting tcf-driven luciferase activity.

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Accordingly, Applicants respectfully submit that the claims do have written description in the specification, and thus request withdrawal of the Examiner's rejection.

In paragraph 4, on page 5 of the Office Action, the Examiner maintains the rejection of Claims 71, 73, 75 and 77 under 35 U.S.C. § 102(e) as being anticipated by Tang et al.

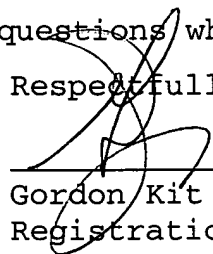
Specifically, it is the Examiner's position that contrary to Applicants' contention, the scope of the claims include a polypeptide which contains both HD1 and HD2 in view of the "or" language.

Again, Claim 71 has been amended to correct the typographical error, i.e., to delete "or" (second occurrence), thereby rendering moot the Examiner's rejection.

Accordingly, Applicants respectfully submit that the present invention is not taught or suggested in Tang et al, and thus request withdrawal of the Examiner's rejection.

The Examiner is invited to contact the undersigned at his Washington telephone number on any questions which might arise.

Respectfully submitted,

  
\_\_\_\_\_  
Gordon Kit  
Registration No. 30,764

**SUGHRUE MION, PLLC**

Telephone: (202) 293-7060

Facsimile: (202) 293-7860

WASHINGTON OFFICE

**23373**

CUSTOMER NUMBER

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